International Committee on Systematic Bacteriology

Subcommittee on the taxonomy of *Mollicutes*

Minutes of the meetings, 21 and 28 July 1998, Sydney, Australia

Session 1. Closed meeting

Minute 1. Call to order. The closed meeting was called to order at 09:00 on 21 July 1998 by the Chair, J. M. Bradbury.

Minute 2. Record of attendance. The members present were J. M. Bové, J. M. Bradbury (Chair), G. Christiansen, G. Firrao, K.-E. Johansson (Secretary), B. C. Kirkpatrick, F. Laigret, J. D. Pollack, S. Razin, J. A. Robertson, K. Sachse and R. H. Leach (advisory member). *Ex-officio* members present were M. K. Davidson and J. K. Davis of the University of Florida, D. G. Pitcher of the Public Health Laboratory Service, London, and F. C. Minion, Chair of the Board of the International Research Programme on Comparative Mycoplasmaology (IRPCM) of the International Organization for Mycoplasmaology (IOM). Apologies for absence were received from J. Frey, R. J. Miles, H. C. Neimark, R. F. Rosenbusch, D. Taylor-Robinson, J. G. Tully and R. F. Whitcomb.

Minute 3. Report of the Chair. J. M. Bradbury welcomed two new subcommittee members, G. Firrao from Italy and K. Sachse from Germany, to the meeting. Two other new members, J. Frey from Switzerland and R. F. Rosenbusch, were unable to attend. The untimely death of I. Kahane was noted with great regret and his valuable contributions to the subcommittee were acknowledged by all. The subcommittee received the resignation of J. Maniloff.

Three new *Mycoplasma* species (*Mycoplasma crocodyli*, *Mycoplasma lagogenitalium*, *Mycoplasma sturni*) and one *Candidatus* species (*Mycoplasma ravigulmonis*) were validly published during the last biennium. The species name *Mycoplasma leocaptivus* was changed to *Mycoplasma leonicaptivi* as suggested by Trüper & de' Clari [Int J Syst Bacteriol 48 (1998), 615]. Fifteen new *Spiroplasma* species (*Spiroplasma alleghenense*, *Spiroplasma chrysopicola*, *Spiroplasma corruscae*, *Spiroplasma diabroticae*, *Spiroplasma gladiatoris*, *Spiroplasma helicoides*, *Spiroplasma lampyridicola*, *Spiroplasma leptinotarsae*, *Spiroplasma lineolae*, *Spiroplasma litorale*, *Spiroplasma montanense*, *Spiroplasma platyhelix*, *Spiroplasma syrphidicola*, *Spiroplasma tabanidicola*, *Spiroplasma turonicum*) were published and a manuscript describing a further *Spiroplasma* species is in press. This group of mollicutes has recently been reclassified. A manuscript describing a new *Entomoplasma* species and another describing a new phytoplasma *Candidatus* species are in press. J. M. Bradbury expressed thanks to the secretary of the subcommittee for organizing the meeting agenda and to J. G. Tully for a considerable amount of helpful advice and information. I. Humphrey-Smith and the organizing committee of the 13th International Congress of the IOM were also thanked for their assistance in making the arrangements for the subcommittee meetings.

Minute 4. *Spiroplasma* reclassification. J. M. Bové reported on the classification and reclassification of spiroplasmas. There are now 40 named and five potential new species of

Spiroplasma. A revision of the group classification of spiroplasmas has been introduced and a few errors in a previous classification have been corrected and recently reported by D. L. Williamson *et al.* [Int J Syst Bacteriol 48 (1998), 1–12]. Based on serological data, new spiroplasma groups have been introduced and some groups have been further divided into subgroups. Currently, the genus *Spiroplasma* consists of 34 groups. Group I was previously divided into eight subgroups and group VIII and group XVI have now been divided into three subgroups. A spiroplasma (*S. poulsonii*) isolated from fruit flies (*Drosophila willistoni*) has shown some serological reactions with representatives of group I, but has now been assigned to group II spiroplasmas. The above revisions in the classification of the genus *Spiroplasma* were based on more than 3300 serological reactions; it will be difficult in the future to undertake studies on this scale for the introduction of new species into the current classification scheme. F. Laigret reported that many 16S rDNA sequences of spiroplasmas have been determined although they were not yet available in the databases. The possibility of using 16S rRNA sequence analysis as an alternative to serology was discussed, but it was concluded that such sequencing data are probably unsuitable due to the very high sequence similarity found between representatives of certain species.

Minute 5. *Phytoplasma* taxonomy. B. C. Kirkpatrick reported on the current status of phytoplasma taxonomy. A manuscript has been prepared which proposes the use of the major 16S rRNA clades for a definition of the genus *Phytoplasma* as a *Candidatus*. Papers describing putative species based on the major clades within the genus *Phytoplasma* would then follow. However, such a scheme would present some major problems because organisms with very different biological properties would be given the same *Candidatus* species name. This could raise problems; hence it may be more appropriate to use the pathovar designation for the time being. The possibility of using a subspecies designation for a grapevine phytoplasma from Australia was also discussed. A review in which the general properties of the '*Candidatus* Phytoplasma' genus is described was recently published by E. Seemüller *et al.* [J Plant Pathol 80 (1998), 3–26]. At present 20 groups of phytoplasmas have been described.

Minute 6. Taxonomy of the *Mycoplasma mycoides* cluster. K.-E. Johansson summarized some recent work on the phylogeny of members of the *Mycoplasma mycoides* cluster. Little has been done during the previous biennium to elucidate the taxonomy of this cluster. The DNA–DNA hybridization studies performed by R. J. Miles and co-workers are not yet complete. Sequence analyses of the 16S rRNA genes from approximately 25 strains of *Mycoplasma capricolum* subsp. *capripneumoniae* and approximately 20 strains of *Mycoplasma mycoides* subsp. *mycoides* SC have been done. Members of these two subspecies show very characteristic sequence patterns and can be differentiated

unambiguously from the other members of the *Mycoplasma mycoides* cluster by 16S rDNA sequence analysis. *Mycoplasma capricolum* subsp. *capripneumoniae* was found to be a very heterogeneous subspecies whereas *Mycoplasma mycoides* subsp. *mycoides* SC is very homogeneous with respect to 16S rRNA sequences. However, the sequences of more strains from the other members of the *Mycoplasma mycoides* cluster need to be determined, although it will probably not be possible to differentiate *Mycoplasma mycoides* subsp. *capri* from *Mycoplasma mycoides* subsp. *mycoides* LC by this method. The usefulness of DNA–DNA hybridization was also discussed; it was concluded that the method is a valuable tool in taxonomy because it reflects the relatedness between whole genomes and not single genes. However, one should be aware of the problems with reproducibility and hybridization values of around 70 %, the latter represent a grey zone around the species level cut-off value [Stackebrandt, E. & Goebel, B. M. (1994). *Int J Syst Bacteriol* **44**, 846–849]. DNA–DNA hybridization techniques are not much used for mollicutes at present.

Minute 7. *Ureaplasma urealyticum* and '*Ureaplasma parvum*'. J. A. Robertson described the differences between *U. urealyticum* and '*U. parvum*' strains; a manuscript on this issue will soon be submitted for publication. There are many phenotypic and genotypic differences between members of these taxa, including sequence differences in genes for rRNA, urease and multiple-banded antigen (MBA). Preliminary data suggest that '*U. parvum*' strains may be more pathogenic than those assigned to *U. urealyticum*; several laboratories are currently evaluating this observation. Strain 27, serovar 3 standard, which has been used in the comparison of *U. urealyticum* and '*U. parvum*', was isolated by D. Ford and has been distributed to a number of researchers. This strain has also been used in the ureaplasma genome sequencing project. Unconfirmed information indicates that the company which supports the genome project is trying to take out a patent on the genome sequence. Strain 27 is still available from J. A. Robertson, as well as from the ATCC and NCTC. The problem of loss of pathogenicity and corresponding genes in strains which have been cultivated for a long time was discussed. It was mentioned that some *U. urealyticum* strains have lost up to 25 % of their genomes.

Minute 8. Impact of antigenic and genetic variation on diagnosis of mollicutes. K. Sachse initiated a discussion on antigenic and genetic variation within the mollicutes. Antigenic variation has been reported for many mollicutes. The consequence of this variation on diagnostics had been discussed within Working Group II of the European COST action 826 on 'Ruminants' Mycoplasmoses'; K. Sachse was asked to summarize the group's conclusions. Numerous phenotypes may be present in a mycoplasma population and cloning may introduce a bias towards certain of them. A number of recommendations has been worked out by the group in an attempt to take into account phenotypic and genotypic diversification among mycoplasma strains and to enable meaningful comparison of diagnostic findings within the Working Group. These recommendations, which can be obtained from K. Sachse, involve some new definitions, suggestions for maintenance and propagation of strains and advice about serological detection methods, reagents and DNA-based detection. The recommendations were particularly relevant to diagnostic work, but it would seem impossible to avoid filter cloning when characterizing members of a new species because primary isolates may fall into more than one species. However, after filter cloning, it would be desirable to pick a set of colonies for further

characterization and also to keep track of the number of passages of the different clones.

Minute 9. *Mycoplasma bovis* and *Mycoplasma agalactiae*. S. Razin initiated a discussion on the similarity between *Mycoplasma bovis* and *Mycoplasma agalactiae*, the former was once regarded as a subspecies of *Mycoplasma agalactiae*. Members of both species are important from a clinical viewpoint as they cause diseases in different animals, but their 16S rRNA sequences are 99.8 % similar. K.-E. Johansson pointed out that the intraspecific variations in the 16S rRNA genes of *Mycoplasma bovis* and *Mycoplasma agalactiae* are comparatively great, but so far it has always been possible to differentiate between members of these species by sequence analysis. J. Frey has shown that the gene (*uvrC*) of the DNA-repair enzyme can be used as a target for PCR primers to distinguish between members of the two species. The DNA–DNA reassociation value of 40 % [Stackebrandt, E. & Goebel, B. M. (1994). *Int J Syst Bacteriol* **44**, 846–849] was used as an argument to classify the two organisms as different species; K. Sachse pointed out that these experiments have been repeated in the laboratory of H. Kirchhoff. These data, which have yet to be published, support the recognition of *Mycoplasma bovis* and *Mycoplasma agalactiae* as distinct species. It has also been found recently that only part of the *vsp* system of *Mycoplasma bovis* is present in *Mycoplasma agalactiae*. However, members of the two species have many antigens in common.

Minute 10. The new edition of *Bergey's Manual of Systematic Bacteriology*. A written statement from J. G. Tully, who is an editor of Volume III of the next edition of *Bergey's Manual of Systematic Bacteriology*, indicated that the new edition will contain less descriptive but more tabular data on recognized species. It will also appear as an electronic version thereby allowing the manual to be updated more frequently than in the past. The mollicutes will be included in Volume III together with other bacteria that have a low G + C content in their genomes.

Minute 11. Taxonomy of Mollicutes and GenBank. The species names given to mollicutes in protein and nucleic acid sequence databases are not always up to date. K.-E. Johansson reported some errors to GenBank and the corresponding entries have now been revised. F. Laigret will contact the administrators of RDP and the rRNA WWW server to get some other entries updated. It is important that researchers who have deposited sequences in databases also help the relevant administrators to keep the entries updated.

Minute 12. Phylogenetic markers additional to 16S rRNA. A general consensus was that 16S rRNA genes are the first choice phylogenetic marker, but this is sometimes not sufficient for species definition. The possibility of using a set of conserved genes (up to 50) for phylogenetic purposes was discussed and the following markers were considered: ITS-regions, ribosomal protein genes, *tuf* genes, *ftsZ* genes, the β -operon (containing genetic information for four ribosomal proteins and RNA polymerases) and heat-shock protein genes. It was suggested that the selection of suitable genes might be a goal for the IRPCM. However, much more work is needed to evaluate the usefulness of genes other than 16S rRNA genes as phylogenetic markers.

Minute 13. Sterol utilization as a taxonomic criterion for mollicutes other than members of the genus *Acholeplasma*. F. Laigret introduced a taxonomic problem that involved the genera *Entomoplasma* and *Mesoplasma*. The order *Entomoplasmatales* is divided into two taxa, the families

Entomoplasmataceae and *Spiroplasmataceae*; this division is in general agreement with the corresponding 16S rRNA-based phylogeny. The family *Entomoplasmataceae* encompasses the genera *Entomoplasma* and *Mesoplasma*, members of which can be distinguished on the basis of sterol utilization (or rather Tween 80; if it can be used as a substitute for sterols in a serum-free medium). However, this division does not correlate well with phylogenetic data based on 16S rDNA sequence analysis. Similar observations have been made for spiroplasmas, where at least four species do not require sterol for growth, but the differentiation is not supported by phylogenetic data. Thus, it appears to be only the acholeplasmas whose non-sterol requirement is phylogenetically supported. The possibility to unify *Entomoplasma* and *Mesoplasma* spp. into a single genus was discussed. The name *Entomoplasma* will hopefully be adopted, because all the organisms in question have insect hosts and the genus *Entomoplasma* appears to have priority over the genus *Mesoplasma*. This matter requires further discussion, especially among the authors of the publication which proposed the establishment of these genera [J. G. Tully *et al.* *Int J Syst Bacteriol* **43** (1993), 378–385].

Minute 14. Enzymic analysis for the assignment of generic affiliation amongst mollicutes. J. D. Pollack reported on a study from his group on the distribution of functional enzymes amongst the mollicutes. Part of the study has been published [J. D. Pollack *et al.* (1997). *Crit Rev Microbiol* **23**, 269–354]. Members of 29 species, representing all eight genera, were selected and about 300 different enzymic assays were performed with most of these strains. All of the strains lacked cytochromes, and the TCA and Embden–Meyerhof cycles. Hence they are unique amongst prokaryotes. The question then arises whether a useful classification scheme, based on different enzymic activities, can be designed for the differentiation of the genera within the mollicutes. A number of useful enzymic activities were found. Pyrophosphate-dependent phosphofructokinase (PP_i-PFK) is potentially useful because members of *Acholeplasma* and *Anaeroplasma* spp. (and *Mesoplasma florum*) have a PP_i-PFK. Members of all of the other genera have a PFK which is not PP_i-dependent; instead they utilize ATP. The enzyme dUTPase was found to be useful for the differentiation of *Acholeplasma* spp. from *Mesoplasma florum* strains; acholeplasmas have this enzyme but *Mesoplasma florum* does not. Spiroplasmas and *Mycoplasma mycoides* subsp. *mycoides* SC strains produce dUTPase thereby supporting the close relationship found between these taxa on the basis of 16S rRNA sequence analysis. Entomoplasmas, mesoplasmas and mycoplasmas (except members of the *Mycoplasma mycoides* cluster) lack a dUTPase. No enzyme was found to unambiguously differentiate *Entomoplasma*, *Mesoplasma* and *Mycoplasma* spp. However, deoxyguanosine kinase was present in most *Entomoplasma*, *Mesoplasma* and *Spiroplasma* spp. but was absent in *Mycoplasma* spp., except for *Mycoplasma fermentans* and *Mycoplasma hominis*. The test for the reduction of benzyl viologen was found to be both simple and very useful for identifying members of the *Acholeplasma* genus, since *Acholeplasma* spp. are positive. Two enzymes which are highly conserved in mollicutes were chosen for cloning and sequence analysis, namely phosphoglycerate kinase (PGK), which is thought to be a major source of ATP in mollicutes, and hypoxanthine-(guanine) phosphoribosyltransferase. Sequence analysis of the enzymes and their genes were used to establish phylogenetic inferences. In preliminary studies, the sequence of the PGK gene from *Mycoplasma fermentans* was found to be more

similar to the corresponding sequence from *Mycoplasma capricolum* subsp. *capricolum* than to those of other members of the phylogenetic hominis group. Thus, genes coding for the 16S rRNA molecule and PGK may have evolved at different rates. The conclusions were that the enzyme analysis scheme is useful for classification and for primary identification, and that it has phylogenetic relevance.

Minute 15. Sequencing of 16S rDNA from mollicutes. The genus *Mycoplasma* accommodates 106 species validly described and four illegitimate names. If 16S rRNA sequence analysis is to be used as a complementary tool for describing new species, a necessary prerequisite is that the 16S rRNA sequences of representatives of all recognized species be available in GenBank. Currently about 70 16S rRNA sequences are available for *Mycoplasma* species. A project designed to determine the sequences of representatives of the remaining species was outlined by K.-E. Johansson; to date 30 new 16S rRNA sequences have been determined, the remaining 10 will shortly be completed. All of these sequences will soon be available from GenBank. A document containing a compilation of all of the accession numbers in GenBank for all of these rRNA sequences is available upon request from K.-E. Johansson. When all of the 16S rRNA sequences are available for all of the mollicute genera it will be possible to determine to which phylogenetic cluster [as defined by Weisburg *et al.* (1989). *J Bacteriol* **171**, 6455–6467] members of potentially new species belong. It should then only be necessary to test isolates against antisera to members of the relevant clusters. This approach will facilitate the future description of new species. Many new 16S rRNA sequences from the genus *Spiroplasma* were presented in a preliminary report at the IOM meeting by D. E. Dodge and co-workers.

Minute 16. Taxonomy of uncultivable animal mollicutes: *Haemobartonella* spp. and *Eperythrozoon* spp. Written statements from H. Neimark and J. G. Tully were read and discussed. In summary: in 1979, R. F. Whitcomb suggested (*The Mycoplasmas*, vol. III) that the wall-less *Haemobartonella* spp. and *Eperythrozoon* spp. (haemotrophic bacteria) should be further studied, because they might be considered as putative mollicutes. In 1997, Y. Rikihisa and co-workers (*J Clin Microbiol* **35**, 823–829) performed sequence analysis of the 16S rRNA genes of *Haemobartonella muris*, *Haemobartonella felis* and *Eperythrozoon suis* and concluded that these species are mollicutes with the closest sequence similarity to *Mycoplasma imitans*, *Mycoplasma pirum* and *Mycoplasma muris* (of the deposited sequences). In 1997, H. Neimark and K. M. Kocan (*FEMS Microbiol Lett* **156**, 287–291) showed that *Eperythrozoon wenyonii* is closely related to the mollicutes of the phylogenetic pneumonias group as defined by Weisburg and co-workers. *Haemobartonella* spp. and *Eperythrozoon* spp. are currently placed in the family *Anaplasmataceae* in the order *Rickettsiales*. They are uncultivable, wall-less bacteria of 300–500 nm in diameter which are inhibited by tetracyclines, but resistant to penicillin. They are closely associated with red blood cells of animals in which anaemia is sometimes a feature, particularly after splenectomy. Blood-sucking insects, including ticks, have been implicated in transmission. The subcommittee considered that the above species should be reclassified, but the responsibility is that of the authors involved.

Minute 17. Minimum standards document. D. G. Pitcher initiated a brief discussion on the difficulties encountered by workers attempting descriptions of new species due to the extensive serological tests required. However, this issue was

already partly covered under Minutes 4, 14 and 15, hence it was decided that it was not necessary to update the Minimum Standards document at this stage. If 16S rRNA sequencing was introduced as a tool in defining new species, the method should be adopted by everyone describing a new species, as a potentially new species would have to be compared with all other sequences of recognized species within the relevant genus.

Minute 18. Liaison with IRPCM. F. C. Minion reported on the activities of the IRPCM, which currently consists of 13 working teams organized according to species or subject area. The main achievements within the different teams since the previous meeting were: whole genome sequencing of *Mycoplasma pneumoniae* and *Ureaplasma urealyticum*, clarification of the molecular mechanisms for the adhesion of members of species other than *Mycoplasma pneumoniae* and the establishment of a Web site (<http://mycoplasmas.vmi.ia-state.edu/IRPCM/irpcm.html>) for easy retrieval of information about the activities of the IRPCM. Future needs have been identified, including the continuous validation of different diagnostic procedures. The IRPCM can also play an important role in the co-ordination of genome sequencing projects.

Minute 19. Status of the NIAID and NCTC mollicute reference collection. M. K. Davidson reported on the status of the mycoplasma culture collection of the University of Florida. Most antisera have been transferred from NIAID and the mycoplasma strains of NIAID will be transferred during 1999. R. F. Whitcomb has donated his *Spiroplasma* strains. J. A. Robertson will supply the antisera against *Ureaplasma* spp. and D. G. Pitcher will also make his culture collection available. One goal is to establish a Web site for the mycoplasma culture collection of the University of Florida. The cost for an order will be \$30 to cover the expenses for shipment and the like.

Minute 20. Future meetings. The next meeting of the subcommittee will be held in conjunction with the IOM meeting in Fukuoka, Japan (14–19 July 2000). The meeting in year 2002 will take place in Vienna, Austria.

Minute 21. Election of officers and membership changes. R. Harasawa from Japan was elected as a new member of the subcommittee.

Minute 22. Any other business. It was generally agreed that more time will be needed to discuss issues at the next meeting of the subcommittee. The allocation of more time would also enable invitations to be made to other experts who might wish to participate in the closed meeting.

Minute 23. Adjournment. The closed meeting was adjourned at 12:30 on 21 July 1998.

Session 2. Open meeting

Minute 24. Call to order. An open meeting of the subcommittee was called to order at 14:15 on 28 July 1998 by the Chair, J. M. Bradbury.

Minute 25. Record of attendance. The members present were J. M. Bové, J. M. Bradbury (Chair), G. Firrao, K.-E. Johansson (Secretary), R. Harasawa, B. C. Kirkpatrick, F. Laigret, J. D. Pollack, J. A. Robertson and K. Sachse. Also present were *ex-officio* members M. K. Davidson and J. K. Davis.

Minute 26. J. M. Bradbury welcomed approximately 30 attendees to the meeting and explained that the purpose of

the meeting was to summarize the main discussions of the closed meeting of the subcommittee. She explained that the subcommittee on the taxonomy of *Mollicutes* is not affiliated to the IOM but to the International Committee on Systematic Bacteriology. The untimely death of I. Kahane was reported and his valuable contributions to subcommittee business were acknowledged.

Minute 27. *Spiroplasma* reclassification. A synopsis of *spiroplasma* reclassification was presented by J. M. Bové. The 45 validly described species of the genus *Spiroplasma* have been divided into 34 groups and several subgroups.

Minute 28. *Phytoplasma* taxonomy. B. C. Kirkpatrick summarized the discussions which had taken place on *phytoplasma* taxonomy and the problems involved in the definition of new species within this group of mollicutes.

Minute 29. *Ureaplasma urealyticum* and *Ureaplasma parvum*. J. A. Robertson reported that the two biovars of *U. urealyticum* show five clear phenotypic differences and five genotypic differences in addition to differences in the sequences of the 16S rRNA genes, elongation factor genes and the urease gene.

Minute 30. Impact of antigenic and genetic variation on diagnosis. K. Sachse summarized the 'Recommendations to avoid phenotypic and genotypic diversification of mycoplasma strains' which had been drawn up within the European COST Action 826 on Ruminants' Mycoplasmoses.

Minute 31. Problems with GenBank. K.-E. Johansson reported on the updating of GenBank with respect to some entries related to mollicutes, which were not correct. The importance of keeping GenBank updated was emphasized.

Minute 32. Phylogenetic markers additional to 16S rRNA genes. J. M. Bradbury, in summarizing the earlier discussions, reported that the subcommittee agreed that a new definition of species is needed, but that conserved genes other than 16S rRNA should be used as additional markers. Several possibilities were discussed, but it appeared to be too early to take a decision in light of current knowledge. There was a general feeling that the best approach would be to refer the problem to the Molecular Genetics Team of IRPCM.

Minute 33. Sterol requirement as a taxonomic criterion for mollicutes other than *acholeplasmas*. F. Laigret summarized the reasons for suggesting that the genera *Entomoplasma* and *Mesoplasma* be combined into one genus, namely *Entomoplasma*. The division into two genera is not supported by phylogenetic analysis and it could be risky to base taxonomy simply on the ability of these organisms to grow in the presence of Tween 80.

Minute 34. Enzymic analysis for the assignment of generic affiliation among mollicutes. It was generally accepted that for the moment a polyphasic taxonomy embracing the best phenotypic, genotypic and phylogenetic information should be used to determine generic affiliations amongst mollicutes. With this in mind, J. D. Pollack and co-workers have developed an enzymic scheme by which mollicutes can be differentiated.

Minute 35. Update on 16S rDNA sequencing of mollicutes. K.-E. Johansson summarized the current status of 16S rRNA sequencing of mollicutes. Most 16S rDNA sequences of representatives of species from the genus *Spiroplasma* have now been determined; the results were presented by D. E. Dodge at the 12th IOM meeting. Sequencing of the 16S rRNA genes from all members of the genus *Mycoplasma* is

almost completed and the results will be presented before or at the next IOM meeting. A compilation of accession numbers to the rRNA sequences of mollicutes of the genus *Mycoplasma* in GenBank is available upon request from K.-E. Johansson.

Minute 36. *Eperythrozoon* spp. and *Haemobartonella* spp. Written statements were received from H. Neimark and J. G. Tully suggesting that the haemotrophic bacteria should be reclassified as mollicutes. Discussions are in progress with various taxonomic experts to determine the best approach to the eventual reclassification of these organisms. The subcommittee can make recommendations, but cannot take responsibility for renaming, which must be done by specialists.

Minute 37. Reference collections. The status of the mycoplasma culture collection of the University of Florida was summarized. By April 1999, the culture collection of J. G. Tully will have been transferred to the University of Florida. The culture collection of R. F. Whitcomb has been transferred to the University of Florida. Minimal funding is available to maintain the Florida reagents, but reagent requirements have been prioritized.

Minute 38. Election of Officers. R. Harasawa has been elected to fill the vacancy on the subcommittee.

Minute 39. Current membership. The current membership of the subcommittee is as follows: J. M. Bradbury, Liverpool, UK (Chair); K.-E. Johansson, Uppsala, Sweden (Secretary); J. M. Bové, Villenave d'Ornon, France; G. Christiansen, Aarhus, Denmark; J. Frey, Berne, Switzerland; G. Firrao, Udine, Italy; R. Harasawa, Tokyo, Japan; B. C. Kirkpatrick, Davis, CA, USA; F. Laigret, Villenave d'Ornon, France; R. J. Miles, London, UK; H. C. Neimark, NY, USA; J. D. Pollack, Columbus, OH, USA; S. Razin, Jerusalem, Israel; J. A. Robertson, Edmonton, Canada; R. F. Rosenbusch, Ames, IA, USA; K. Sachse, Jena, Germany; J. G. Tully, Frederick, MD, USA; R. F. Whitcomb, Patagonia, AZ, USA. Advisory members are E. A. Freundt, Højebjerg, Denmark; R. H. Leach, Radlett, UK; D. Taylor-Robinson, Buckinghamshire, UK. *Ex officio* members are F. C. Minion, Ames, IA, USA (IOM IRPCM Chair); M. K. Davidson and J. K. Davis, Gainesville, FL, USA; and D. G. Pitcher, London, UK.

Minute 40. Adjournment. J. M. Bradbury thanked everyone who attended the open meeting and contributed to the discussions. The open meeting was adjourned at 15:10 on 28 July 1998.

K.-E. Johansson, *Secretary*